

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1-13. (canceled)

14. (currently amended) A method for the ~~enzymatic~~ production of L-amino acids ~~in~~ using coryneform bacteria comprising:

- a) ~~fermenting, in a medium, the coryneform bacteria which produce the a desired L-amino acid and in which at least the sigC gene or nucleotide sequences coding for the latter are enhanced~~ comprising an overexpressed polynucleotide sigC wherein said polynucleotide comprises a nucleotide sequence of SEQ ID NO:1 and encodes a polypeptide having an RNA polymerase sigma-C factor activity.

15. (canceled)

16. (currently amended) The method according to claim ~~15~~ 14, further comprising:

- e) isolating the L-amino acid.

17. (currently amended) The method according to claim 14, wherein the L amino acids ~~are~~ acid is lysine.

18. (currently amended) ~~The method according to claim 14, wherein coryneform bacteria in which at least the sigC gene or nucleotide sequences coding for the latter are~~

~~overexpressed are fermented~~ A method for the production of L-amino acids using coryneform bacteria comprising:

fermenting coryneform bacteria which produce a desired L-amino acid comprising an overexpressed polynucleotide sigC wherein said polynucleotide encodes a polypeptide comprising an amino acid sequence of SEQ ID NO:2.

19-20. (canceled)

21. (original) The method according to claim 14, wherein a strain transformed with a plasmid vector is used, and the plasmid vector carries the nucleotide sequence coding for the sigC gene.

22-24. (canceled)

25. (currently amended) The method according to claim 14, wherein the bacteria being fermented comprise, at the same time, one or more genes which are ~~enhanced~~ overexpressed; wherein the one or more genes is/are selected from the group consisting of:

~~the~~ gene dapA coding for dihydrodipicolinate synthase,
~~the~~ gene gap coding for glyceraldehyde-3-phosphate dehydrogenase,
~~the~~ gene tpi coding for triosephosphate isomerase,
~~the~~ gene pgk coding for 3-phosphoglycerate kinase,
~~the~~ gene zwf coding for glucose-6-phosphate dehydrogenase,
~~the~~ gene pyc coding for pyruvate carboxylase,
~~the~~ gene mgo coding for malate-quinone-oxidoreductase,

~~the~~ gene lysC coding for a feedback-resistant aspartate kinase,
~~the~~ gene lysE coding for a protein for lysine export,
~~the~~ gene hom coding for homoserine dehydrogenase,
~~the~~ gene ilvA coding for threonine dehydratase or ~~the~~ allele ilvA(Fbr) coding
 for a feedback-resistant threonine dehydratase,
~~the~~ gene ilvBN coding for acetohydroxy acid synthase,
~~the~~ gene ilvD coding for dihydroxy acid dehydratase, and
~~the~~ gene zwal coding for ~~the~~ Zwa1 protein.

26. Process according to claim 14, wherein the bacteria being fermented comprise, at the same time, one or more genes which are ~~attenuated~~ eliminated; wherein the genes are selected from the group consisting of:

~~the~~ gene pck coding for phosphoenol pyruvate carboxykinase,
~~the~~ gene pgi coding for glucose-6-phosphate isomerase,
~~the~~ gene poxB coding for pyruvate oxidase, and
~~the~~ gene zwa2 coding for ~~the~~ Zwa2 protein.

27. (currently amended) The method according to claim 14 wherein ~~microorganisms~~ the
bacteria of the genus is Corynebacterium glutamicum ~~are used~~.

28. (currently amended) The method according to claim 27, wherein the Corynebacterium
 glutamicum is a strain of DH5 α mcr/pEC-XK99EsigCb2ex ~~is used~~.

29. (currently amended) The method according to claim 27, wherein the Corynebacterium
 glutamicum is a strain of DSM5715/pEC-XK99E ~~is used~~.

30-32. (canceled)